Feature differences between top and bottom vasculature

in retina fundus images

Louis HEAU
Bertille BOURG
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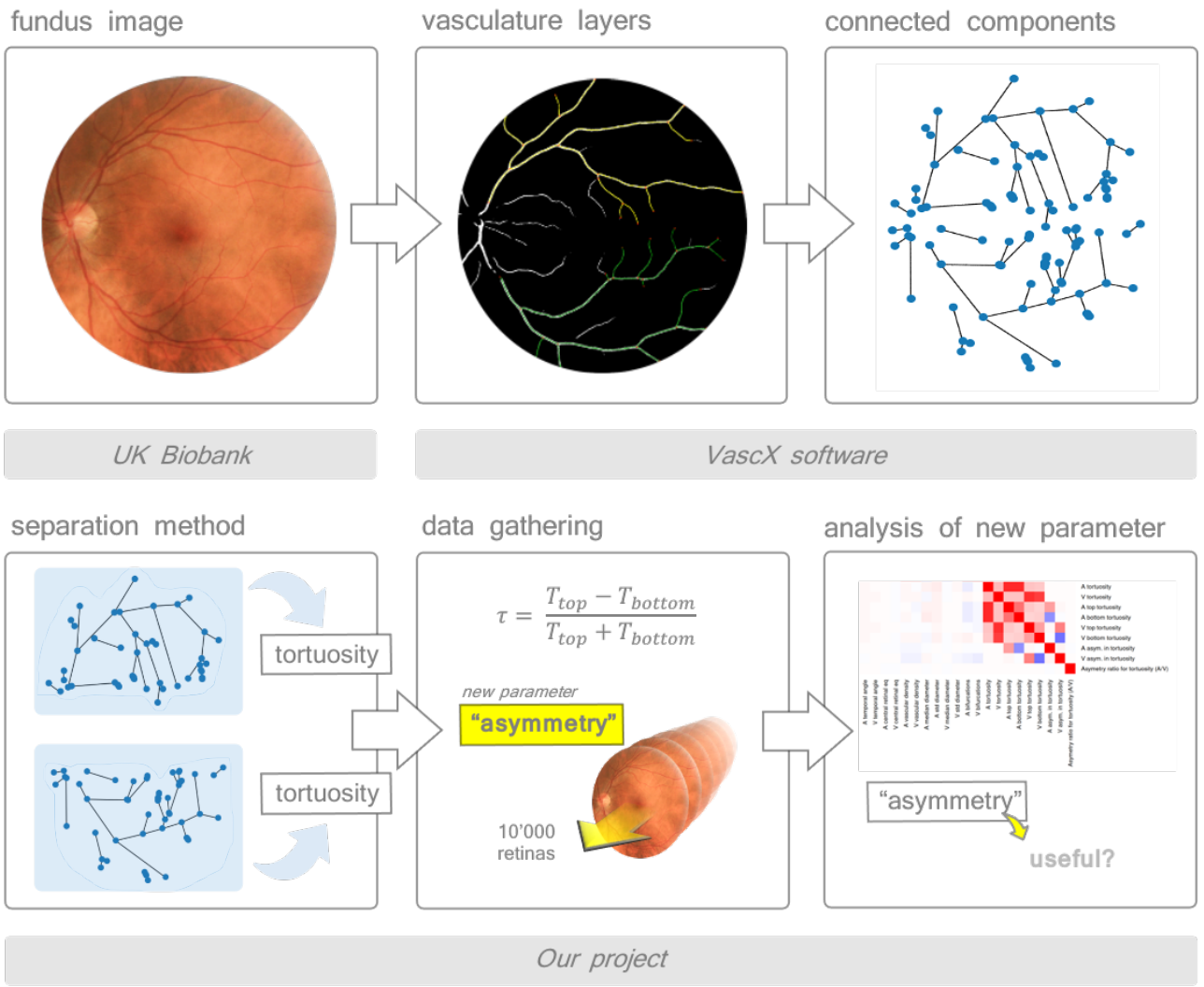
Supervisor: Sacha BORS



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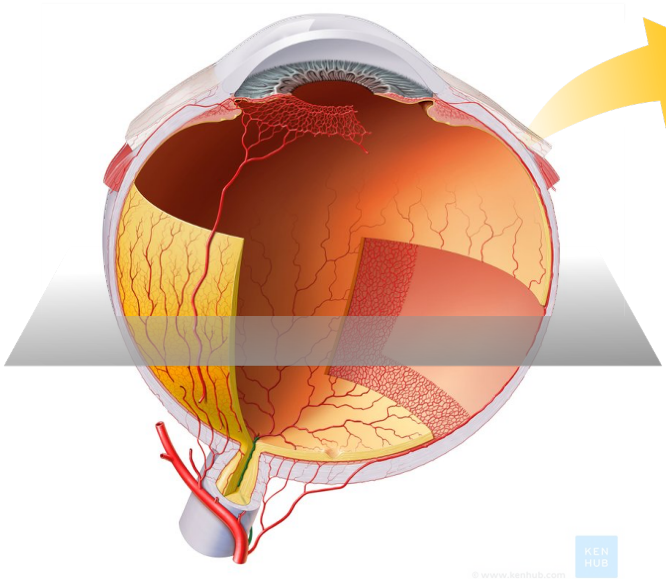
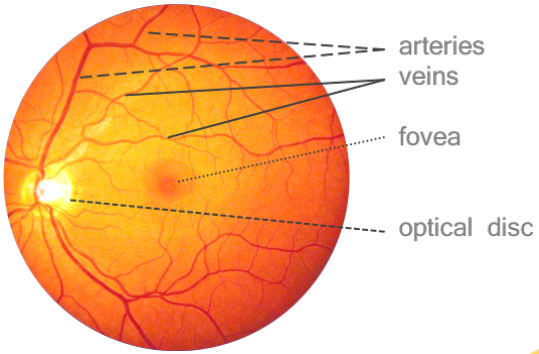
Retina fundus images are processed by a python software, vascX





retina fundus image

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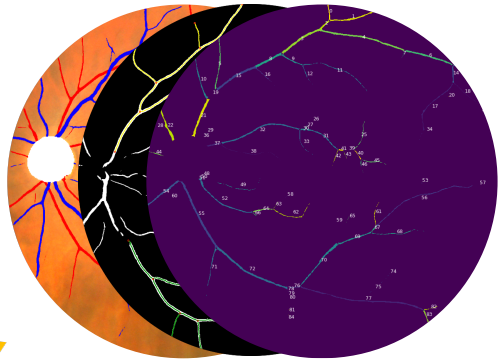
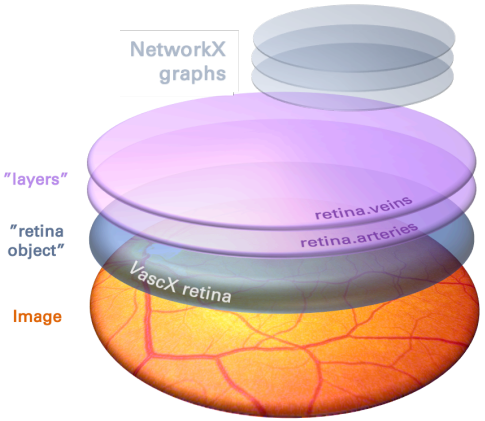


segmentation with the software VascX (python)



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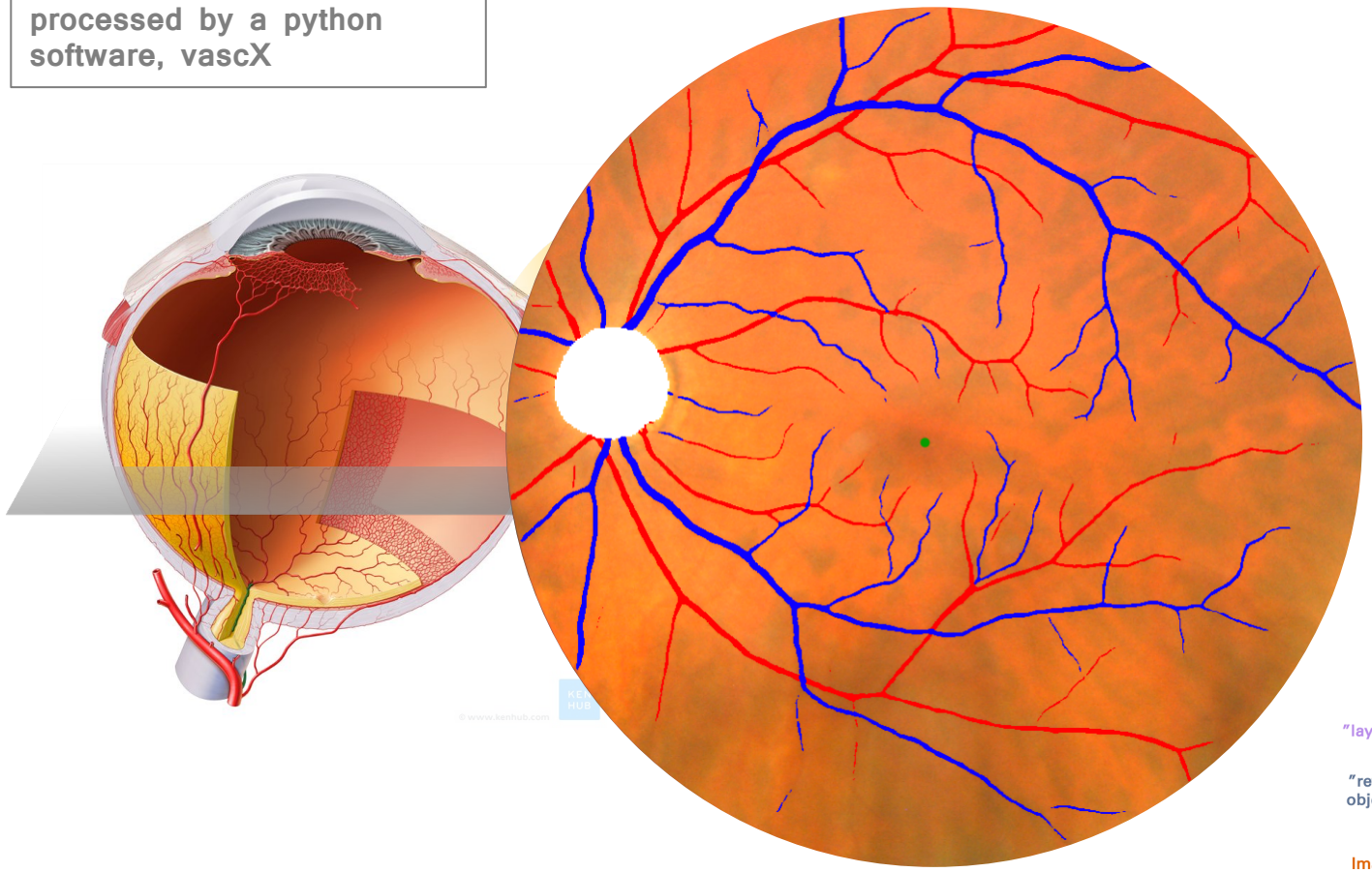

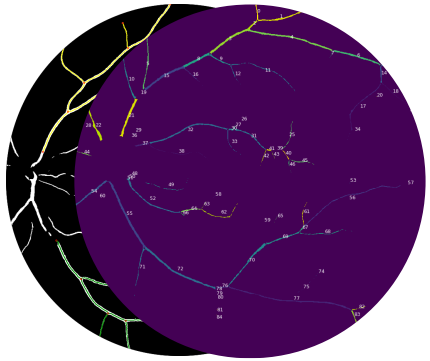

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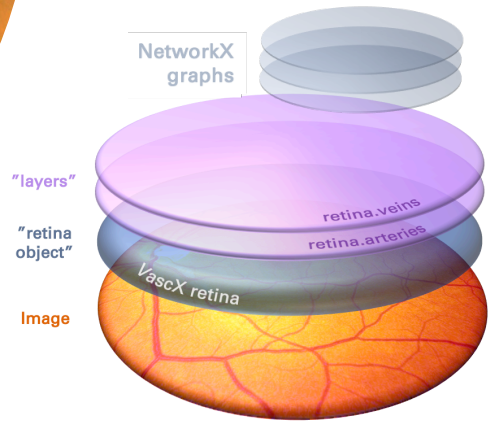

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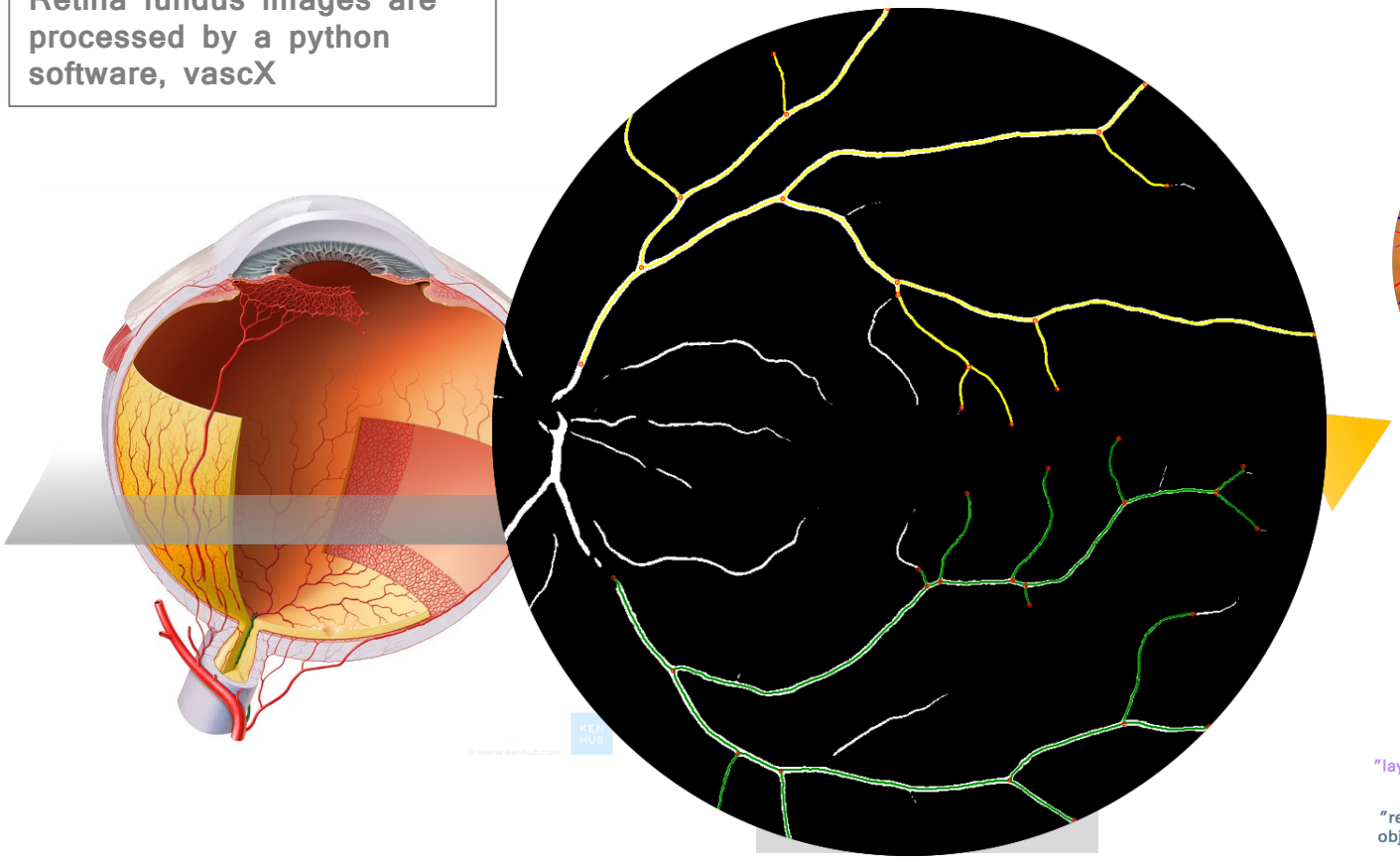

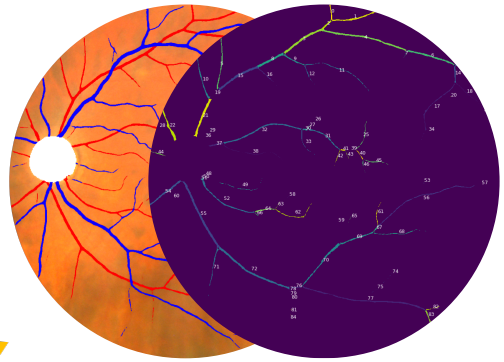

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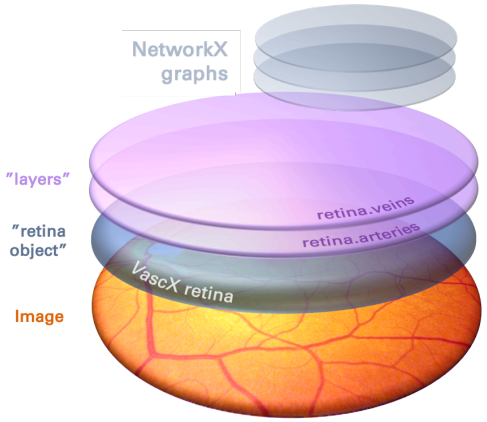

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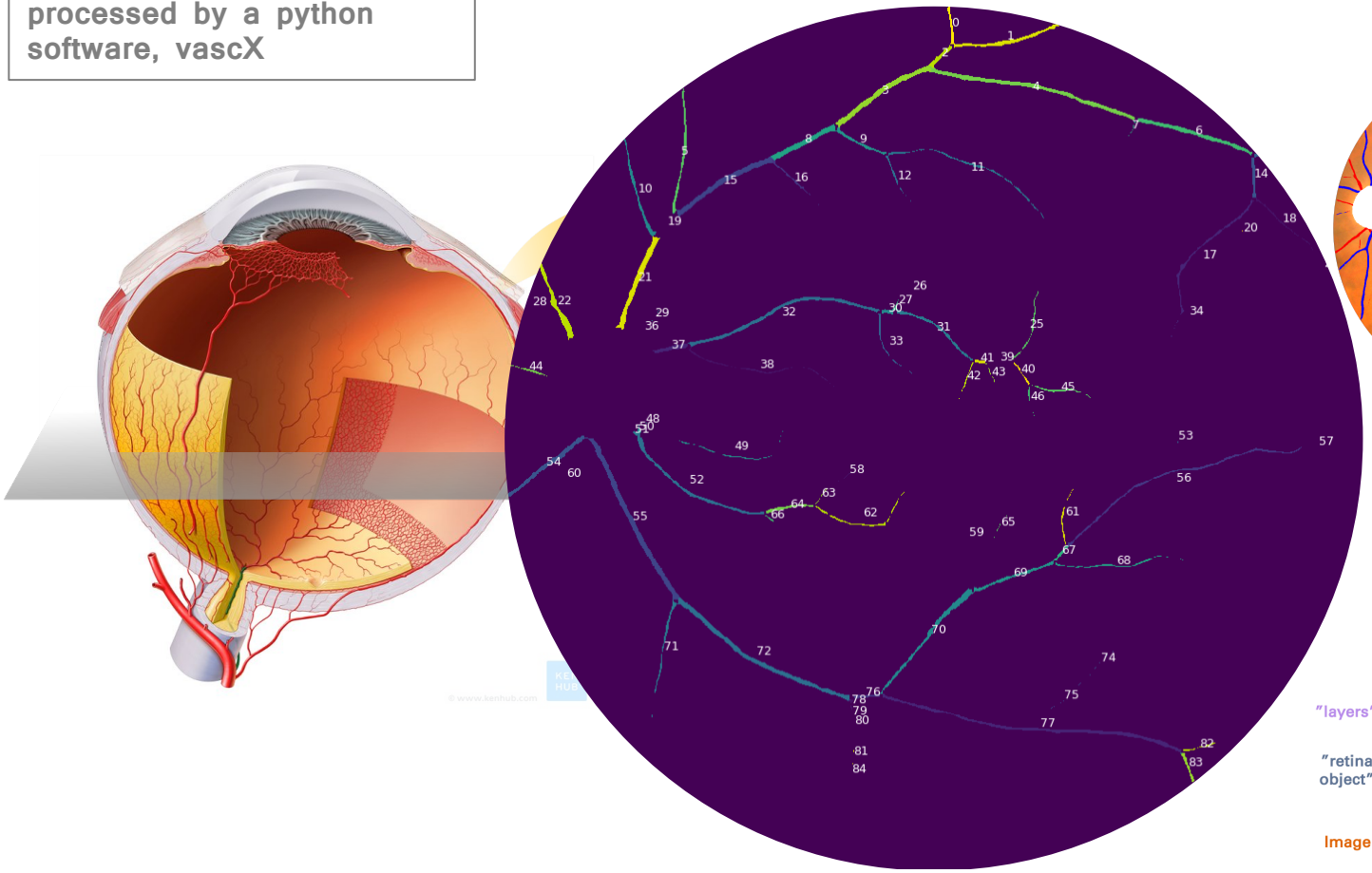

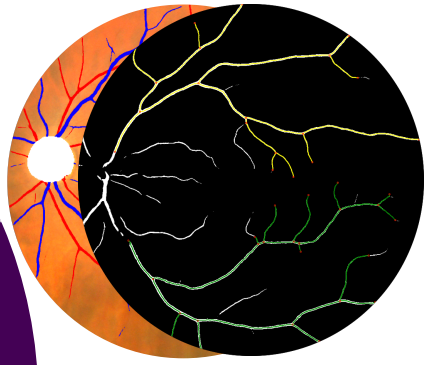

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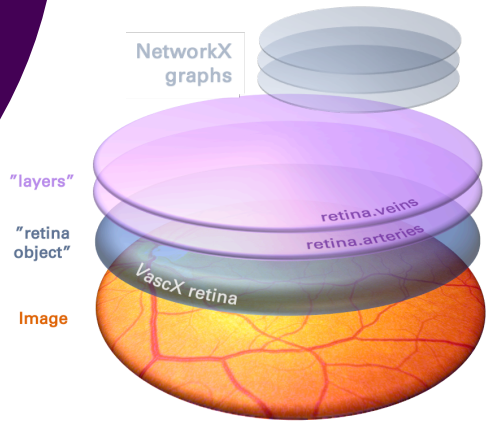

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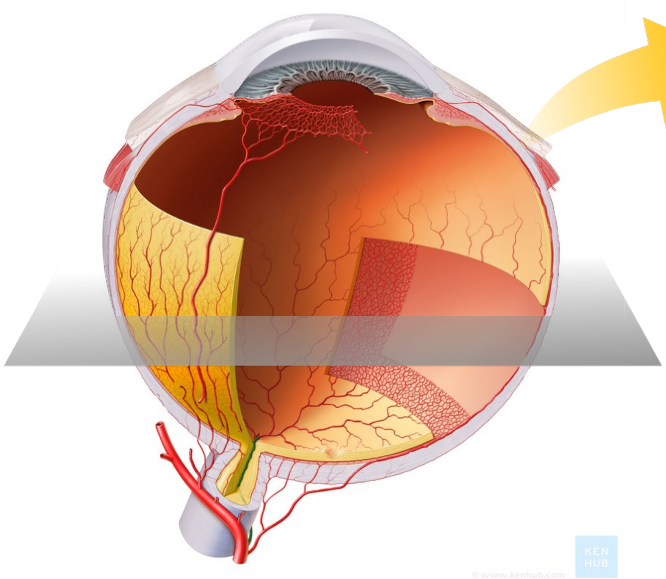

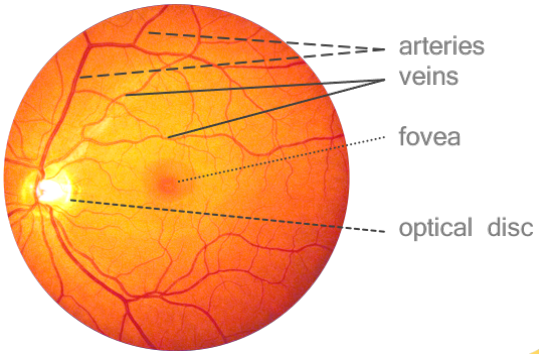

retina fundus image

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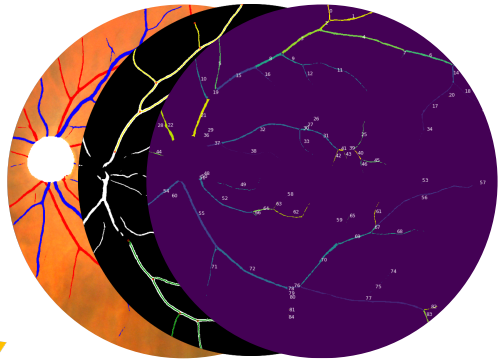

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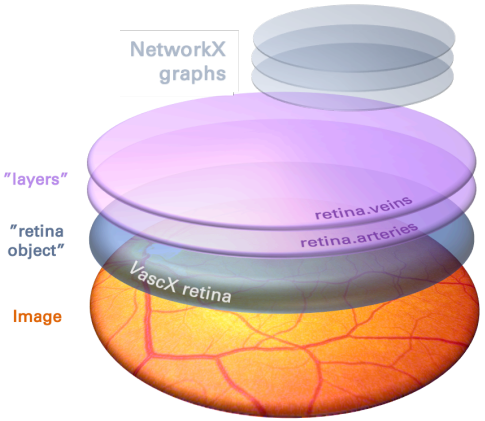

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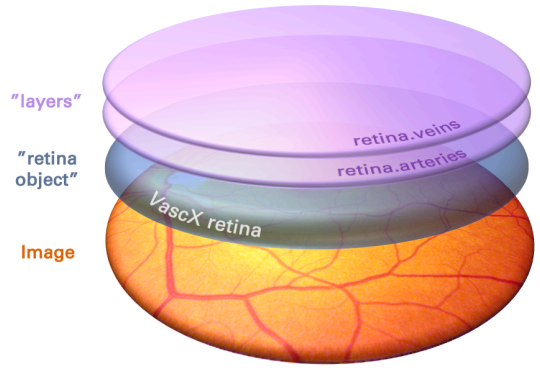
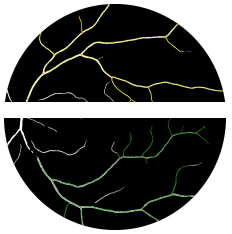
We want to know if there is a different tortuosity value for each hemisphere within each vessel layer



retina.veins



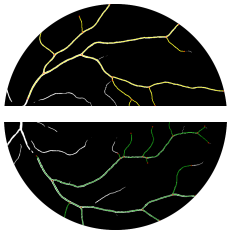
top tortuosity (veins)

bottom tortuosity (veins)

asymmetry

useful?

retina.arteries



top tortuosity (arteries)

bottom tortuosity (arteries)

asymmetry

Separate top and bottom → Calculate tortuosity for each hemisphere → Calculate the asymmetry between the two hemispheres → Determine if the trait is correlated to other known characteristics to see if it's worth it

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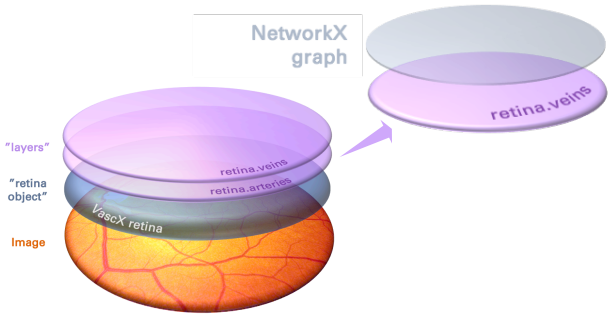
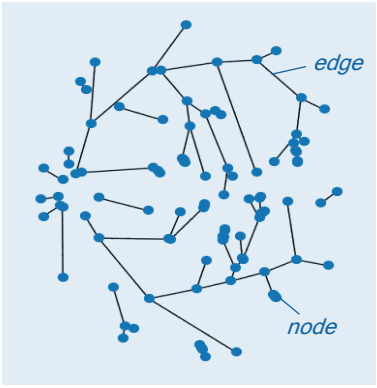
Using the graph representation of the vasculature from the retina object, we need to separate the “nodes” and ”edges” to the TOP or BOTTOM





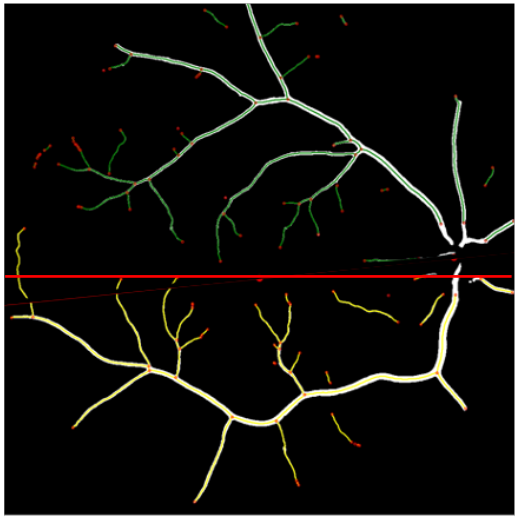
graph

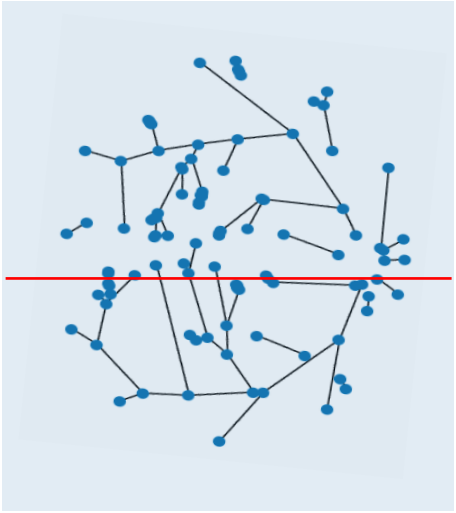
Method 1: “dumb separation”

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$

600 px

1’200 px





if *edge above y = 600*
add edge to “TOP”

else *add edge to “BOTTOM”*

global tortuosity = tortuosity(all edges)

top tortuosity = tortuosity(“TOP”)

bottom tortuosity = tortuosity(“BOTTOM”)

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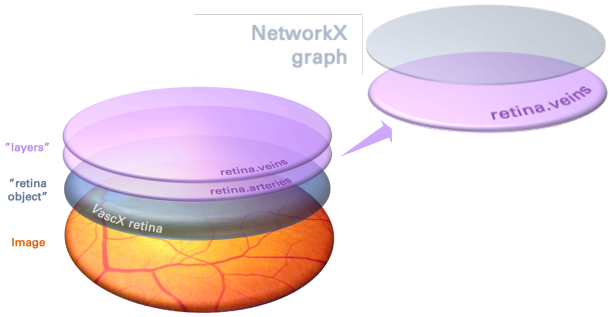
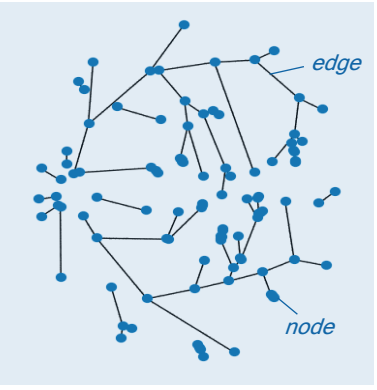
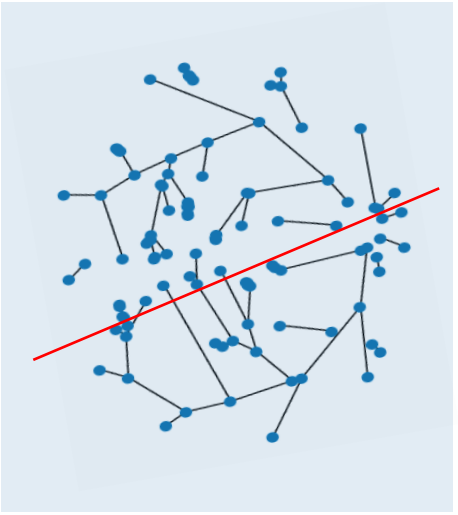




graph

Method 2: Biological anchor points

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$



if *edge above y = mx + b*
add edge to “TOP”

else *add edge to “BOTTOM”*

global tortuosity = tortuosity(all edges)

top tortuosity = tortuosity(“TOP”)

bottom tortuosity = tortuosity(“BOTTOM”)

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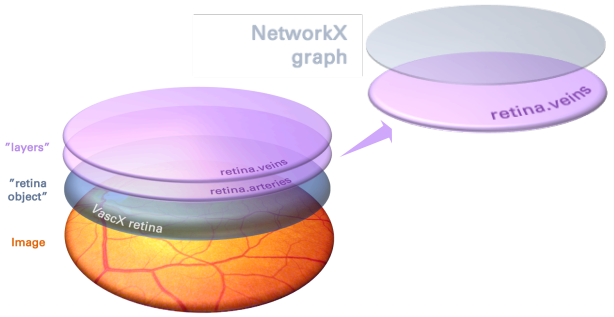
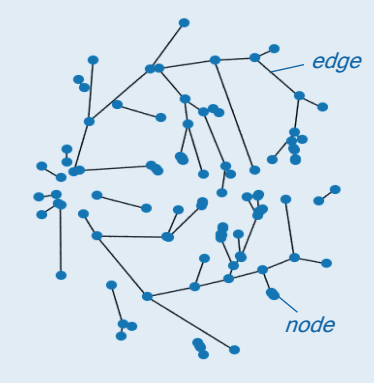
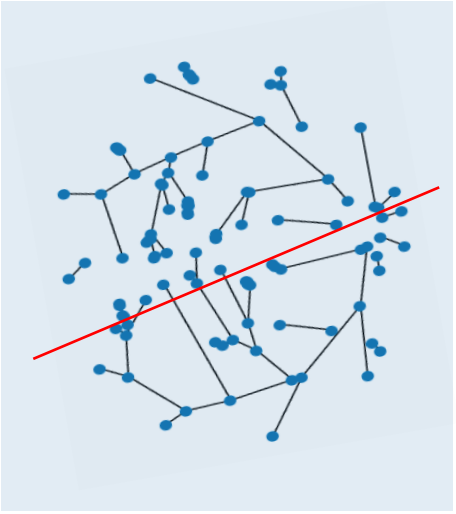




graph

Method 3: Biological anchor points + connected components

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$



nx.connected_components(G)

for *connected component in [...]*

barycentre = (mean(nodes(x)), mean(nodes(y))

if *barycentre above y = mx + b*

add connected component to “TOP”

else *add connected component to “BOTTOM”*

global tortuosity = tortuosity(all edges)

top tortuosity = tortuosity(“TOP”)

bottom tortuosity = tortuosity(“BOTTOM”)

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Method 3: Biological anchor points + connected components

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if *barycentre above y = mx + b*

add connected component to "TOP"

else *add connected component to "BOTTOM"*

global tortuosity = tortuosity(all edges)

top tortuosity = tortuosity("TOP")

bottom tortuosity = tortuosity("BOTTOM")

retina.veins *list of all top tortuosities*
list of all bottom tortuosities

retina.arteries *list of all top tortuosities*
list of all bottom tortuosities

***control** : fuse and* random.shuffle *then re-assign to top/bottom*

median / sd *of the lists, **asymmetry** values*

Repeat for x retinas

actual algorithm

retina

*calculate **fovea - optical disc** equation*

retina.veins
retina.arteries

*in **retina.veins***

calculate global tortuosity
make dictionnary retina.veins.graph.**edges** → segment *object*

*go in **retina.veins.graph***

make dictionnary connected component → *TOP/BOTTOM*

in dictionnary 'TOP'

[...] list of all top tortuosities

for *connected component in 'TOP'*

for *edge in connected component*

- *find back its segment object*
- *calculate the tortuosity value for the seg.*
- *append it to the top tortuosity list*

in dictionnary 'BOTTOM'

[...]

*in **retina.arteries***

[...]

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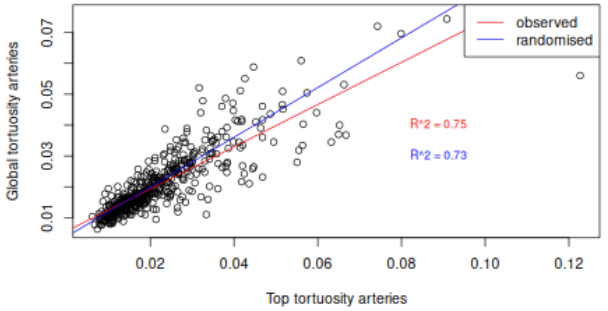
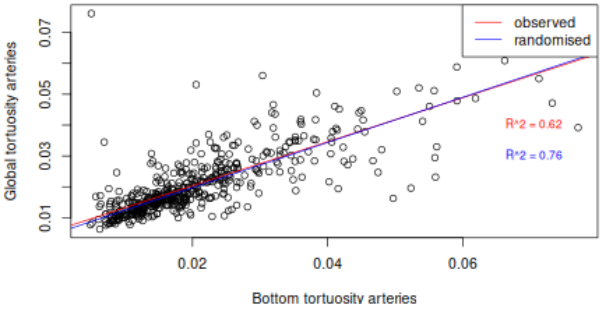
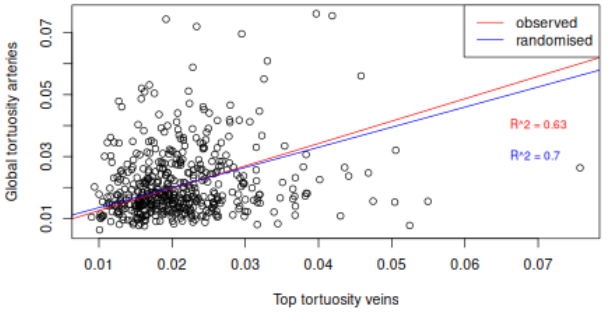
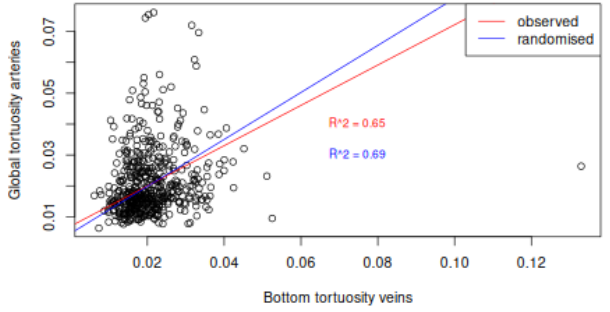
Is the tortuosity for only top/bottom so different than the global tortuosity ? → linear regressions (each point is one retina)

500 retinas

	global vs top	*global vs bottom*
arteries		
veins		

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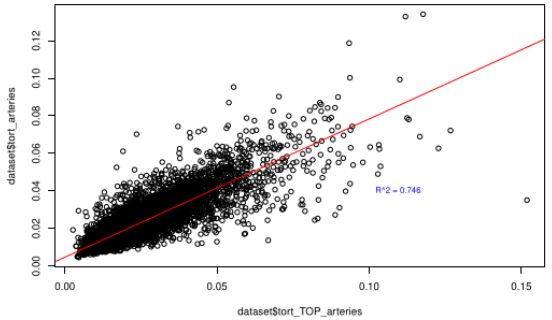
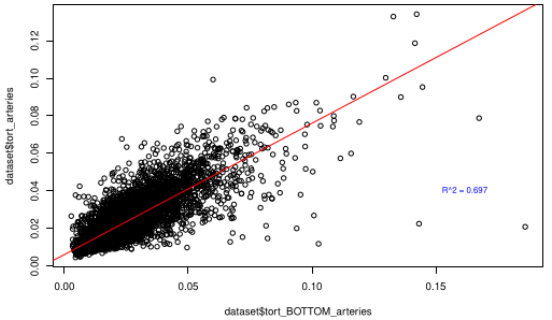
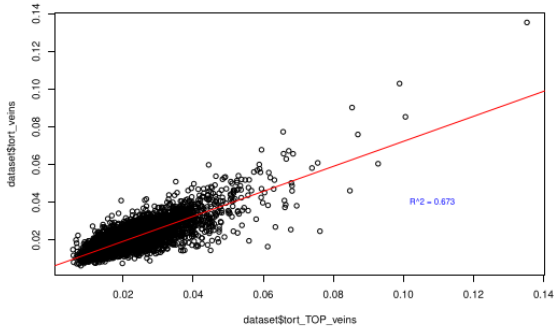
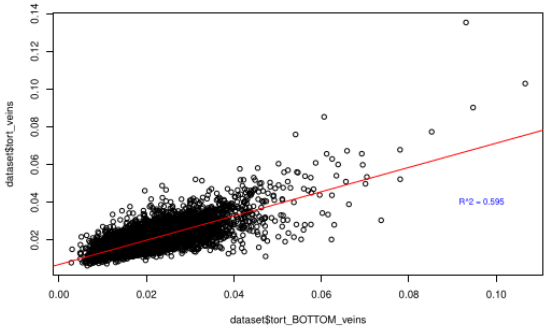
10’000 retinas

	global vs top	*global vs bottom*
arteries		
veins		

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Is the tortuosity for only top/bottom so different than the global tortuosity ? → linear regressions (each point is one retina)

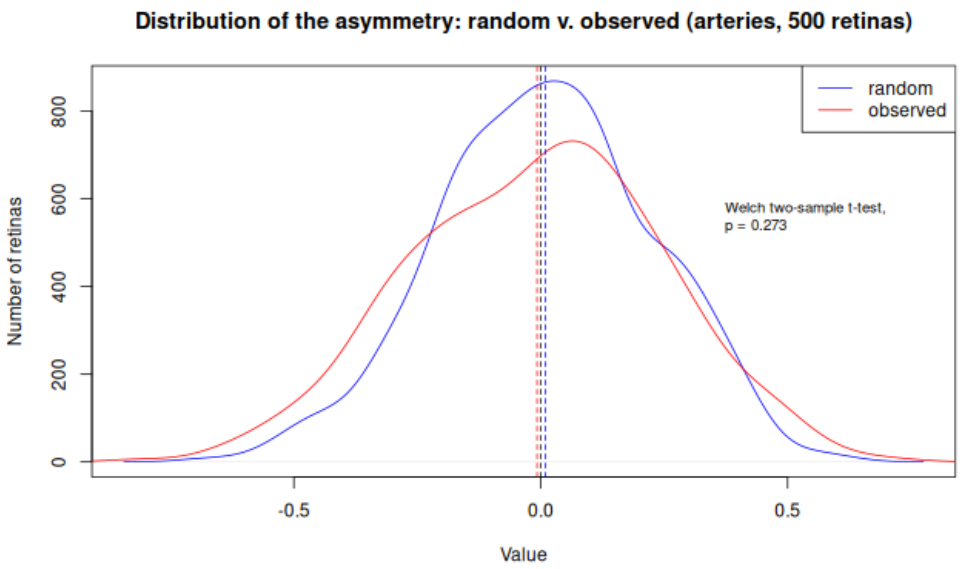
it appears so

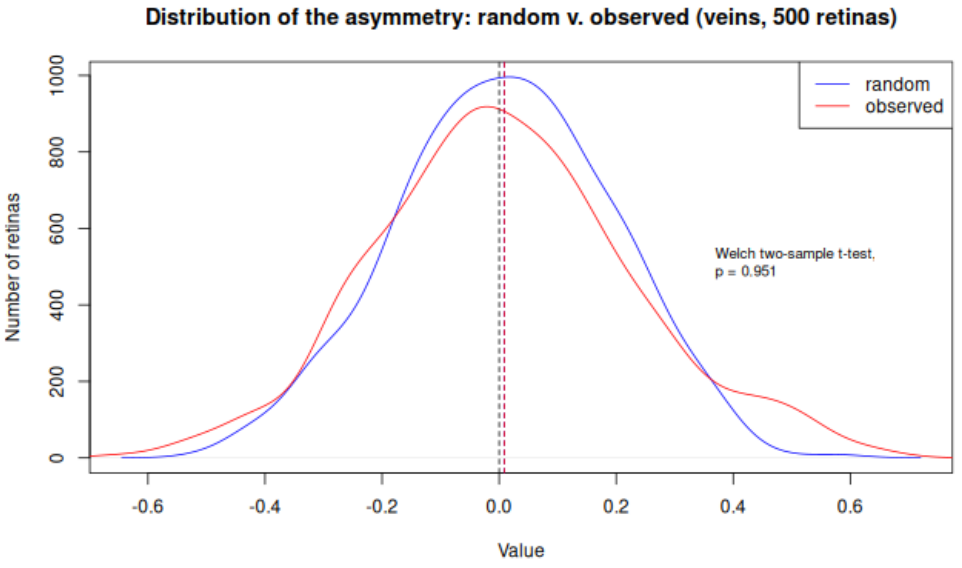
calculate an asymmetry coefficient

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$

we can plot the distribution of the asymmetries observed vs randomized to see if there is a significant effect

The asymmetry could as well have been randomly generated?





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Is the tortuosity for only top/bottom so different that the top tortuosity ? → linear regressions (each point is one retina)

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calculate an asymmetry coefficient

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$

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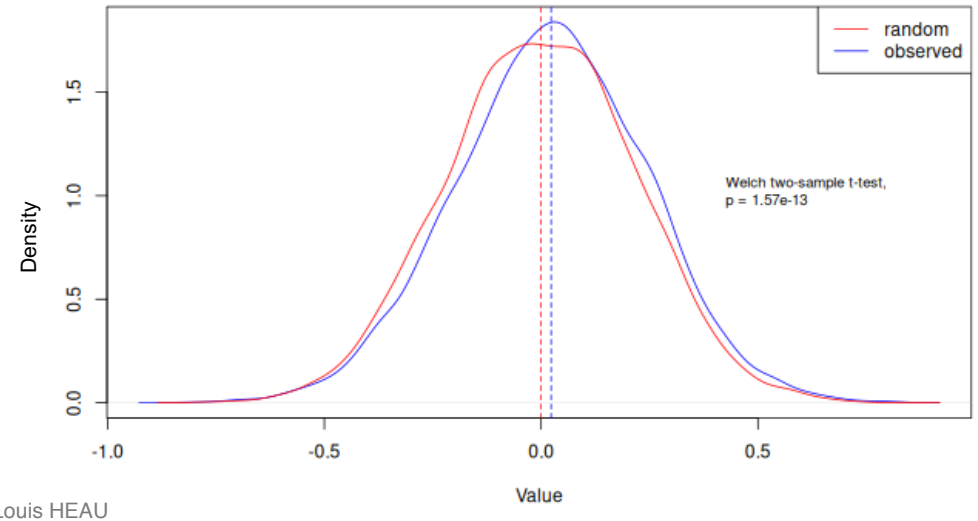
Distribution of the asymmetry: random v. observed (arteries, 10'000 retinas)



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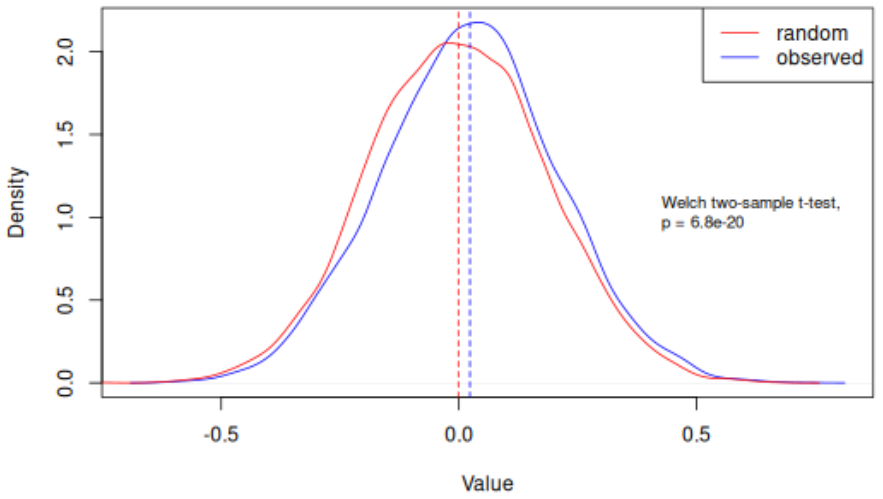

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new “asymmetry” value which seems to encode the existing difference between the top and bottom tortuosities

is it correlated with other traits that have been calculated ? If it is it’s not useful we could just take the other traits…

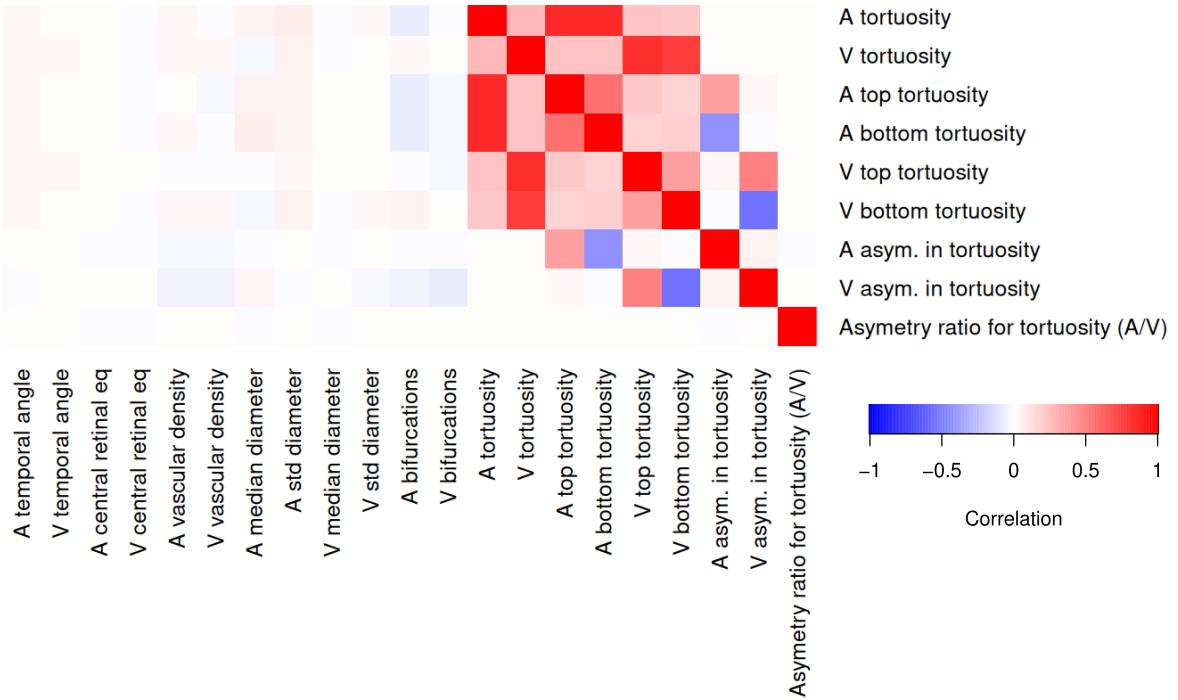
diagonal ✓

coherent with the formula ✓

$$\tau = \frac{T_{top} - T_{bottom}}{T_{top} + T_{bottom}}$$

correlated ? ×

Correlation heatmap of tortuosity traits



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Asymmetry

- Genetic factors?
  → GWAS
- Environment?
  → Sun?
  → Diseases

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Thank you!

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